

# SEQUENCE LISTING

<110> Union Chimique Belge, S.A.  
Nocka, Karl  
Pirozzi, Gregory  
Einstein, Richard

<120> NOVEL GENES ASSOCIATED WITH ALLERGIC HYPERSENSITIVITY AND MAST CELL ACTIVATION

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ccc cgc gcc ccg gac gca cag gag ccg gag gag gac gag gcc ggc gcg Pro Arg Ala Pro Asp Ala Gln Glu Pro Glu Glu Asp Glu Ala Gly Ala 80 85 90	652
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acc ggc ggt ccc acc cga aag atg ccc ccc agc gcc agt gcc gtg gac Thr Gly Gly Pro Thr Arg Lys Met Pro Pro Ser Ala Ser Ala Val Asp 110 115 120	748
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cag aca aac atg tat gcc aag aag ttc cag gag cgg ttt ggg agc gac Gln Thr Asn Met Tyr Ala Lys Lys Phe Gln Glu Arg Phe Gly Ser Asp 145 150 155	844
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cgc tcc agc cag acc acg cac ggg ctc tac aag gtc cag ccc ttc ctc Arg Ser Ser Gln Thr Thr His Gly Leu Tyr Lys Val Gln Pro Phe Leu 225 230 235	1084
gac tcc ctg cag aac agc ttc gac tct gcc ttc agg cct tcc caa acc Asp Ser Leu Gln Asn Ser Phe Asp Ser Ala Phe Arg Pro Ser Gln Thr 240 245 250	1132
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acg tgc aca gag cgg gag ctg cga aag agg aaa aag cgg aaa ttc agc	1228
Thr Cys Thr Glu Arg Glu Leu Arg Lys Arg Lys Lys Arg Lys Phe Ser	
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ctc tgg gtc aga caa tgt tct tcc act ggc ttc atc atc cag att tat	1276
Leu Trp Val Arg Gln Cys Ser Ser Thr Gly Phe Ile Ile Gln Ile Tyr	
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Val His Leu Lys Glu Gly Gly Gly Pro Asp Gly Leu Asp Ala Leu Lys	
305 310 315	
aat aag ccc cag ctc cac agc atg gtg gcc agg agc ctg tgc cgg aac	1372
Asn Lys Pro Gln Leu His Ser Met Val Ala Arg Ser Leu Cys Arg Asn	
320 325 330	
gcg gca ggc aag aac tac atc att ttc acg ggg ccc agc atc acc agc	1420
Ala Ala Gly Lys Asn Tyr Ile Ile Phe Thr Gly Pro Ser Ile Thr Ser	
335 340 345	
ctg acg ctg ttt gaa gag ttt gag aag caa ggg att tac tgc tgc ggc	1468
Leu Thr Leu Phe Glu Glu Phe Glu Lys Gln Gly Ile Tyr Cys Cys Gly	
350 355 360	
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Leu Leu Arg Ala Arg Lys Ser Asp Cys Thr Gly Leu Pro Leu Ser Met	
365 370 375 380	
ctg acc aac cca gcc aca ccc ccg gcc cgg ggc cag tac caa atc aag	1564
Leu Thr Asn Pro Ala Thr Pro Pro Ala Arg Gly Gln Tyr Gln Ile Lys	
385 390 395	
atg aag ggg aac atg tcc ttg atc tgc tgg tac aac aaa gga cac ttc	1612
Met Lys Gly Asn Met Ser Leu Ile Cys Trp Tyr Asn Lys Gly His Phe	
400 405 410	
cgc ttc ctg acc aac gcc tac tcc ccg gtg cag cag gga gtc atc atc	1660
Arg Phe Leu Thr Asn Ala Tyr Ser Pro Val Gln Gln Gly Val Ile Ile	
415 420 425	
aaa agg aag agt ggg gag atc cca tgc ccc ttg gcc gtg gag gcg ttt	1708
Lys Arg Lys Ser Gly Glu Ile Pro Cys Pro Leu Ala Val Glu Ala Phe	
430 435 440	
gcc gct cac ctg agc tac atc tgc aga tac gat gac aaa tac agc aag	1756
Ala Ala His Leu Ser Tyr Ile Cys Arg Tyr Asp Asp Lys Tyr Ser Lys	
445 450 455 460	
tat ttc att tct cat aaa cca aac aag acc tgg cag cag gtg ttc tgg	1804
Tyr Phe Ile Ser His Lys Pro Asn Lys Thr Trp Gln Gln Val Phe Trp	
465 470 475	
ttc gcc atc agc atc gcc atc aac aat gcc tac atc ctg tac aaa atg	1852
Phe Ala Ile Ser Ile Ala Ile Asn Asn Ala Tyr Ile Leu Tyr Lys Met	
480 485 490	
tca gac gcc tac cac gtg aag agg tac agc cgg gcg cag ttt gga gag	1900
Ser Asp Ala Tyr His Val Lys Arg Tyr Ser Arg Ala Gln Phe Gly Glu	
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aga ctc gtc aga gag ctg ctg ggc ttg gag gat gcc tct ccg acc cac	1948

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tcaggtgtga	tttgacatga	gggccggagg	cggttgtctg	cggcaggact	ggagaggctg											3141
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<212> PRT  
<213> Homo sapiens  
<400> 7

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Glu Ala Ala Arg Ala Arg Tyr Glu Ser Leu His Ile Ser Asp Asp Val  
20 25 30

Phe Gly Glu Ser Gly Pro Asp Ser Gly Gly Asn Pro Phe Tyr Ser Thr  
35 40 45

Ser Ala Ala Ser Arg Ser Ser Ser Ala Ala Ser Ser Asp Asp Glu Arg  
50 55 60

Glu Pro Pro Gly Pro Pro Gly Ala Ala Pro Pro Pro Pro Arg Ala Pro  
65 70 75 80

Asp Ala Gln Glu Pro Glu Glu Asp Glu Ala Gly Ala Gly Trp Ser Ala  
85 90 95

Ala Leu Arg Asp Arg Pro Pro Pro Arg Phe Glu Asp Thr Gly Gly Pro  
100 105 110

Thr Arg Lys Met Pro Pro Ser Ala Ser Ala Val Asp Phe Phe Gln Leu  
115 120 125

Phe Val Pro Asp Asn Val Leu Lys Asn Met Val Val Gln Thr Asn Met  
130 135 140

Tyr Ala Lys Lys Phe Gln Glu Arg Phe Gly Ser Asp Gly Ala Trp Val  
145 150 155 160

Glu Val Thr Leu Thr Glu Met Lys Ala Phe Leu Gly Tyr Met Ile Ser  
165 170 175

Thr Ser Ile Ser His Cys Glu Ser Val Leu Ser Ile Trp Ser Gly Gly  
180 185 190

Phe Tyr Ser Asn Arg Ser Leu Ala Leu Val Met Ser Gln Ala Arg Phe

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195	200	205
Glu Lys Ile Leu Lys Tyr Phe His Val Val Ala Phe Arg Ser Ser Gln 210 215 220		
Thr Thr His Gly Leu Tyr Lys Val Gln Pro Phe Leu Asp Ser Leu Gln 225 230 235 240		
Asn Ser Phe Asp Ser Ala Phe Arg Pro Ser Gln Thr Gln Val Leu His 245 250 255		
Glu Pro Leu Ile Asp Glu Asp Pro Val Phe Ile Ala Thr Cys Thr Glu 260 265 270		
Arg Glu Leu Arg Lys Arg Lys Lys Arg Lys Phe Ser Leu Trp Val Arg 275 280 285		
Gln Cys Ser Ser Thr Gly Phe Ile Ile Gln Ile Tyr Val His Leu Lys 290 295 300		
Glu Gly Gly Gly Pro Asp Gly Leu Asp Ala Leu Lys Asn Lys Pro Gln 305 310 315 320		
Leu His Ser Met Val Ala Arg Ser Leu Cys Arg Asn Ala Ala Gly Lys 325 330 335		
Asn Tyr Ile Ile Phe Thr Gly Pro Ser Ile Thr Ser Leu Thr Leu Phe 340 345 350		
Glu Glu Phe Glu Lys Gln Gly Ile Tyr Cys Cys Gly Leu Leu Arg Ala 355 360 365		
Arg Lys Ser Asp Cys Thr Gly Leu Pro Leu Ser Met Leu Thr Asn Pro 370 375 380		
Ala Thr Pro Pro Ala Arg Gly Gln Tyr Gln Ile Lys Met Lys Gly Asn 385 390 395 400		
Met Ser Leu Ile Cys Trp Tyr Asn Lys Gly His Phe Arg Phe Leu Thr 405 410 415		
Asn Ala Tyr Ser Pro Val Gln Gln Gly Val Ile Ile Lys Arg Lys Ser 420 425 430		
Gly Glu Ile Pro Cys Pro Leu Ala Val Glu Ala Phe Ala Ala His Leu 435 440 445		

Ser Tyr Ile Cys Arg Tyr Asp Asp Lys Tyr Ser Lys Tyr Phe Ile Ser  
450 455 460

His Lys Pro Asn Lys Thr Trp Gln Gln Val Phe Trp Phe Ala Ile Ser  
465 470 475 480

Ile Ala Ile Asn Asn Ala Tyr Ile Leu Tyr Lys Met Ser Asp Ala Tyr  
485 490 495

His Val Lys Arg Tyr Ser Arg Ala Gln Phe Gly Glu Arg Leu Val Arg  
500 505 510

Glu Leu Leu Gly Leu Glu Asp Ala Ser Pro Thr His  
515 520

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<212> DNA  
<213> Homo sapiens

<220>  
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<222> (162)..(635)  
<223> 1st open reading frame .

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gcttccaaac tcatttttga ataatactag gctacaaaga attacactgt gaattcatta 120

agggtaacac caaatcacta aacagcactg tttgtacaga a atg tcg aaa agc tgt 176  
Met Ser Lys Ser Cys  
1 5

gga aat aat tta gcg gcc att tct gta gga att tcg ctt ctt tta ctc 224  
Gly Asn Asn Leu Ala Ala Ile Ser Val Gly Ile Ser Leu Leu Leu Leu  
10 15 20

tta gtg gtt tgt gga att ggg tgt gtt tgg cac tgg aaa cac cgt gtt 272  
Leu Val Val Cys Gly Ile Gly Cys Val Trp His Trp Lys His Arg Val  
25 30 35

gcc aca cga ttt acc tta ccg agg ttt tta caa agg aga agc agc agg 320  
Ala Thr Arg Phe Thr Leu Pro Arg Phe Leu Gln Arg Arg Ser Ser Arg  
40 45 50

aga aaa gtc tgt act aaa aca ttc ttg ggc ccc cgc atc att ggc tta 368  
Arg Lys Val Cys Thr Lys Thr Phe Leu Gly Pro Arg Ile Ile Gly Leu  
55 60 65

agg cat gaa atc tca gtt gaa acc caa gac cac aaa tct gct gtc agg 416  
Arg His Glu Ile Ser Val Glu Thr Gln Asp His Lys Ser Ala Val Arg  
70 75 80 85

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gga aat aac aca cac gac aac tat gaa aat gtg gaa gca ggt cct ccc Gly Asn Asn Thr His Asp Asn Tyr Glu Asn Val Glu Ala Gly Pro Pro 90 95 100	464
aaa gct aaa gga aaa acc gat aag gaa cta tat gaa aac aca ggg cag Lys Ala Lys Gly Lys Thr Asp Lys Glu Leu Tyr Glu Asn Thr Gly Gln 105 110 115	512
tct aat ttc gag gag cat atc tat gga aat gag aca tct tct gac tat Ser Asn Phe Glu Glu His Ile Tyr Gly Asn Glu Thr Ser Ser Asp Tyr 120 125 130	560
tat aac ttc cag aag cct cgt cct tct gaa gtt cct caa gat gaa gat Tyr Asn Phe Gln Lys Pro Arg Pro Ser Glu Val Pro Gln Asp Glu Asp 135 140 145	608
ata tac att ctt cca gat tca tat tag cttttcaaaa tattgacttt Ile Tyr Ile Leu Pro Asp Ser Tyr 150 155	655
tggtattgga tgataaatat tcaactgtaat ttttcaacag caaagacaag gaatcaaact	715
aaatgttgat caactgtaga ctggataaag aaaatgtggt acacatacac catagaatat	775
tatgcagccg taaaaaaaga acaaaactaa catgggaaca gaaaatcaaa taccacatat	835
tctcacttaa aagtgggagc taaataataa gaacacatgg agagaaggag aggaacaaca	895
gacactgggg cctacttgag ggaggacagt ggaaggaggg agagggttcag ggaaaaaaaa	955
aatatcaggt actatgctta gtacacacat gatgaaataa tctgtacacc aaacccccaa	1015
gtcacaagtg ttctacata acaaacctga acatgtaccc ctgaacataa aattataatt	1075
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ccactcaatc aattaccgat ggtgttgcca gatttatctt cagaaaatat tcctaacagc	1435
cacattattt ctttacttta aaatgtttta atgccccctc tttgcaaaag acataataacc	1495
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cattttatta cctagcttca tatgaaaatg tcttaaattc ccacctaaat gaaaagaaac	1855

tgcccaaatg cctagaacat cacataaggc actaaatgcc tcatgtttta ctgacgggaa 1915  
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 tcatccataa aaaaaaaaaa aaa 1998

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 <213> Homo sapiens

<400> 9

Met Ser Lys Ser Cys Gly Asn Asn Leu Ala Ala Ile Ser Val Gly Ile  
 1 5 10 15

Ser Leu Leu Leu Leu Val Val Cys Gly Ile Gly Cys Val Trp His  
 20 25 30

Trp Lys His Arg Val Ala Thr Arg Phe Thr Leu Pro Arg Phe Leu Gln  
 35 40 45

Arg Arg Ser Ser Arg Arg Lys Val Cys Thr Lys Thr Phe Leu Gly Pro  
 50 55 60

Arg Ile Ile Gly Leu Arg His Glu Ile Ser Val Glu Thr Gln Asp His  
 65 70 75 80

Lys Ser Ala Val Arg Gly Asn Asn Thr His Asp Asn Tyr Glu Asn Val  
 85 90 95

Glu Ala Gly Pro Pro Lys Ala Lys Gly Lys Thr Asp Lys Glu Leu Tyr  
 100 105 110

Glu Asn Thr Gly Gln Ser Asn Phe Glu Glu His Ile Tyr Gly Asn Glu  
 115 120 125

Thr Ser Ser Asp Tyr Tyr Asn Phe Gln Lys Pro Arg Pro Ser Glu Val  
 130 135 140

Pro Gln Asp Glu Asp Ile Tyr Ile Leu Pro Asp Ser Tyr  
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<210> 10  
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 <212> DNA  
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<220>  
 <221> CDS

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<222> (373)..(651)  
 <223> 2nd open reading frame

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 tacaaaggag aagcagcagg agaaaagtct gtactaaaac attcttgggc ccccgcatca 360  
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                   Met Lys Ser Gln Leu Lys Pro Lys Thr Thr Asn Leu Leu  
                   1                  5                  10  
 tca ggg gaa ata aca cac acg aca act atg aaa atg tgg aag cag gtc 459  
 Ser Gly Glu Ile Thr His Thr Thr Thr Met Lys Met Trp Lys Gln Val  
                   15                  20                  25  
 ctc cca aag cta aag gaa aaa ccg ata agg aac tat atg aaa aca cag 507  
 Leu Pro Lys Leu Lys Glu Lys Pro Ile Arg Asn Tyr Met Lys Thr Gln  
                   30                  35                  40                  45  
 ggc agt cta att tcg agg agc ata tct atg gaa atg aga cat ctt ctg 555  
 Gly Ser Leu Ile Ser Arg Ser Ile Ser Met Glu Met Arg His Leu Leu  
                   50                  55                  60  
 act att ata act tcc aga agc ctc gtc ctt ctg aag ttc ctc aag atg 603  
 Thr Ile Ile Thr Ser Arg Ser Leu Val Leu Leu Lys Phe Leu Lys Met  
                   65                  70                  75  
 aag ata tat aca ttc ttc cag att cat att agc ttt tca aaa tat tga 651  
 Lys Ile Tyr Thr Phe Phe Gln Ile His Ile Ser Phe Ser Lys Tyr  
                   80                  85                  90  
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 aactaaatgt tgatcaactg tagactggat aaagaaaatg tggtacacat acaccataga 771  
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 aattaaaata ttaaaaataa ttcactgtga tttttattgt actgatgcca ttcttaatca 1131  
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Ile Thr His Thr Thr Thr Met Lys Met Trp Lys Gln Val Leu Pro Lys  
20 25 30

Leu Lys Glu Lys Pro Ile Arg Asn Tyr Met Lys Thr Gln Gly Ser Leu  
35 40 45

Ile Ser Arg Ser Ile Ser Met Glu Met Arg His Leu Leu Thr Ile Ile  
50 55 60

Thr Ser Arg Ser Leu Val Leu Leu Lys Phe Leu Lys Met Lys Ile Tyr  
65 70 75 80

Thr Phe Phe Gln Ile His Ile Ser Phe Ser Lys Tyr  
85 90

<210> 12  
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 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1662)

<223>

<400> 12

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1 5 10 15

cag ctc ttg ctg gtc aac ctg cta acc ttt ggc ctg gag gtg tgt ttg 96  
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu  
20 25 30

gcc gca ggc atc acc tat gtg ccg cct ctg ctg ctg gaa gtg ggg gta 144  
Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val  
35 40 45

gag gag aag ttc atg acc atg gtg ctg ggc att ggt cca gtg ctg ggc 192  
Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly  
50 55 60

ctg gtc tgt gtc ccg ctc cta ggc tca gcc agt gac cac tgg cgt gga 240  
Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly  
65 70 75 80

cgc tat ggc cgc cgc cgg ccc ttc atc tgg gca ctg tcc ttg ggc atc 288  
Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile  
85 90 95

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Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu  
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ctg tgc ccg gat ccc agg ccc ctg gag ctg gca ctg ctc atc ctg ggc 384  
Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly  
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gtg ggg ctg ctg gac ttc tgt ggc cag gtg tgc ttc act cca ctg gag 432  
Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu  
130 135 140

gcc ctg ctc tct gac ctc ttc cgg gac ccg gac cac tgt cgc cag gcc 480  
Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala  
145 150 155 160

tac tct gtc tat gcc ttc atg atc agt ctt ggg ggc tgc ctg ggc tac 528  
Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr  
165 170 175

ctc ctg cct gcc att gac tgg gac acc agt gcc ctg gcc ccc tac ctg 576  
Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu  
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ggc acc cag gag gag tgc ctc ttt ggc ctg ctc acc ctc atc ttc ctc 624  
Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu  
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acc tgc gta gca gcc aca ctg ctg gtg gct gag gag gca gcg ctg ggc	672
Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly	
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ccc acc gag cca gca gaa ggg ctg tgc gcc ccc tcc ttg tgc ccc cac	720
Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His	
225 230 235 240	
tgc tgt cca tgc cgg gcc cgc ttg gct ttc cgg aac ctg ggc gcc ctg	768
Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu	
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Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg	
260 265 270	
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Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe	
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Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val	
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ccc aga gct gag ccg ggc acc gag gcc cgg aga cac tat gat gaa ggc	960
Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly	
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Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu	
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Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg	
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Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala	
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aca tgc ctg tcc cac agt gtg gcc gtg gtg aca gct tca gcc gcc ctc	1152
Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu	
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Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala	
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tcc ctc tac cac cgg gag aag cag gtg ttc ctg ccc aaa tac cga ggg	1248
Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly	
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gac act gga ggt gct agc agt gag gac agc ctg atg acc agc ttc ctg	1296
Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu	
420 425 430	
cca ggc cct aag cct gga gct ccc ttc cct aat gga cac gtg ggt gct	1344
Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala	
435 440 445	
gga ggc agt ggc ctg ctc cca cct cca ccc gcg ctc tgc ggg gcc tct	1392

Gly	Gly	Ser	Gly	Leu	Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser		
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Ala	Cys	Asp	Val	Ser	Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala		
465					470					475					480		
agg	gtg	gtt	ccg	ggc	cgg	ggc	atc	tgc	ctg	gac	ctc	gcc	atc	ctg	gat	1488	
Arg	Val	Val	Pro	Gly	Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp		
				485					490					495			
agt	gcc	ttc	ctg	ctg	tcc	cag	gtg	gcc	cca	tcc	ctg	ttt	atg	ggc	tcc	1536	
Ser	Ala	Phe	Leu	Leu	Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser		
			500					505					510				
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Ile	Val	Gln	Leu	Ser	Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala		
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ggc	ctg	ggc	ctg	gtc	gcc	att	tac	ttt	gct	aca	cag	gta	gta	ttt	gac	1632	
Gly	Leu	Gly	Leu	Val	Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp		
	530					535					540						
aag	agc	gac	ttg	gcc	aaa	tac	tca	gcg	tag							1662	
Lys	Ser	Asp	Leu	Ala	Lys	Tyr	Ser	Ala									
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 <212> PRT  
 <213> Homo sapiens

<400> 13

Met	Val	Gln	Arg	Leu	Trp	Val	Ser	Arg	Leu	Leu	Arg	His	Arg	Lys	Ala		
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			20					25					30				
Ala	Ala	Gly	Ile	Thr	Tyr	Val	Pro	Pro	Leu	Leu	Leu	Glu	Val	Gly	Val		
		35					40					45					
Glu	Glu	Lys	Phe	Met	Thr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly		
	50					55					60						
Leu	Val	Cys	Val	Pro	Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly		
65					70					75					80		
Arg	Tyr	Gly	Arg	Arg	Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile		
			85						90					95			
Leu	Leu	Ser	Leu	Phe	Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu		
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Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly  
115 120 125

Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu  
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Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala  
145 150 155 160

Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr  
165 170 175

Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu  
180 185 190

Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu  
195 200 205

Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly  
210 215 220

Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His  
225 230 235 240

Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu  
245 250 255

Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg  
260 265 270

Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe  
275 280 285

Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val  
290 295 300

Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
305 310 315 320

Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu  
325 330 335

Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg  
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Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala  
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Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
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Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala  
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Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly  
405 410 415

Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu  
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Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala  
435 440 445

Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser  
450 455 460

Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala  
465 470 475 480

Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp  
485 490 495

Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser  
500 505 510

Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
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Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp  
530 535 540

Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
545 550